

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2004, 18:03:15 ; Search time 19 Seconds  
(without alignments)  
1551.496 Million cell updates/sec

Title: US-09-715-927-6

Perfect score: 2929

Sequence: 1 MTRAGDHNRRQCGCGSLADY.....ACGPDKEVRKENQANTSVV 571

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/FACTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1799	61.1	383	4	US-09-149-476-460 Sequence 460, Ap
2	1336	4.6	591	4	US-09-540-236-2490 Sequence 2490, Ap
3	123.5	4.2	524	2	US-08-928-692-12 Sequence 12, Appl
4	123.5	4.2	524	4	US-09-339-972-12 Sequence 12, Appl
5	117	4.0	490	4	US-09-489-039A-13226 Sequence 13226, A
6	113.5	3.9	329	4	US-09-489-039A-14206 Sequence 14206, A
7	112	3.8	305	4	US-09-252-991A-33032 Sequence 33032, A
8	110	3.8	429	4	US-09-328-352-4392 Sequence 4392, Ap
9	109.5	3.7	470	4	US-09-134-001C-4610 Sequence 4610, Ap
10	108	3.7	330	5	US-08-118-270-19 Sequence 19, Appl
11	108	3.7	330	5	PCT-US93-08528-19 Sequence 19, Appl
12	108	3.7	549	4	US-09-489-039A-8237 Sequence 8237, Ap
13	108	3.7	618	4	US-08-595-553A-2 Sequence 2, Appl
14	108	3.7	618	4	US-09-540-198D-4 Sequence 4, Appl
15	107.5	3.7	491	4	US-09-543-681A-8251 Sequence 8251, Ap
16	107.5	3.7	897	4	US-09-543-681A-4249 Sequence 4249, Ap
17	107	3.7	411	4	US-09-134-001C-3299 Sequence 3299, Ap
18	107	3.7	465	4	US-09-328-352-5222 Sequence 5222, Ap
19	107	3.7	512	4	US-09-540-236-3548 Sequence 3548, Ap
20	104	3.6	534	2	US-09-031-392-4 Sequence 4, Appl
21	104	3.6	534	3	US-09-299-543-4 Sequence 4, Appl
22	104	3.6	534	4	US-09-610-417-4 Sequence 4, Appl
23	103.5	3.5	471	4	US-09-328-314-17 Sequence 17, Appl
24	103	3.5	358	2	US-08-748-485-6 Sequence 6, Appl
25	103	3.5	718	4	US-09-657-960-3 Sequence 3, Appl
26	102.5	3.5	443	4	US-09-489-039A-8166 Sequence 8166, Ap
27	102.5	3.5	529	4	US-09-291-922-28 Sequence 28, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-149-476-460  
; Sequence 460, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23

Sequence 2974, Ap  
Sequence 27018, A  
Sequence 6, Appl  
Sequence 27790, A  
Sequence 5398, Ap  
Sequence 5370, Ap  
Sequence 9866, Ap  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 83, Appl  
Sequence 5502, Ap  
Sequence 3227, Ap  
Sequence 6491, Ap  
Sequence 3105, Ap  
Sequence 26031, A  
Sequence 33, Appl  
Sequence 33, Appl  
Sequence 33, Appl

28 102 3.5 553 4 US-09-134-001C-2974  
29 101.5 3.5 996 4 US-09-252-991A-27018  
30 100.5 3.4 411 3 US-09-236-080-6  
31 100.5 3.4 760 4 US-09-252-991A-27790  
32 100 3.4 319 4 US-09-543-681A-5398  
33 100 3.4 499 4 US-09-134-001C-5370  
34 100 3.4 510 4 US-09-489-039A-9866  
35 99.5 3.4 461 1 US-08-194-338-4  
36 98.5 3.4 411 3 US-09-236-080-2  
37 98.5 3.4 411 3 US-09-336-643A-83  
38 98 3.3 366 4 US-09-134-001C-5502  
39 98 3.3 443 4 US-09-134-001C-3227  
40 98 3.3 772 4 US-09-134-000C-6491  
41 98 3.3 808 4 US-09-134-001C-3105  
42 97.5 3.3 596 4 US-09-252-991A-48031  
43 97.5 3.3 808 2 US-08-629-291A-33  
44 97.5 3.3 808 2 US-08-658-335B-33  
45 97.5 3.3 808 4 US-09-406-640-33

1	EARLIER FILING DATE: 1997-08-22
2	EARLIER APPLICATION NUMBER: 60/056,894
3	EARLIER FILING DATE: 1997-08-22
4	EARLIER APPLICATION NUMBER: 60/056,911
5	EARLIER FILING DATE: 1997-08-22
6	EARLIER APPLICATION NUMBER: 60/056,636
7	EARLIER FILING DATE: 1997-08-22
8	EARLIER APPLICATION NUMBER: 60/056,874
9	EARLIER FILING DATE: 1997-08-22
10	EARLIER APPLICATION NUMBER: 60/056,910
11	EARLIER FILING DATE: 1997-08-22
12	EARLIER APPLICATION NUMBER: 60/056,864
13	EARLIER FILING DATE: 1997-08-22
14	EARLIER APPLICATION NUMBER: 60/056,631
15	EARLIER FILING DATE: 1997-08-22
16	EARLIER APPLICATION NUMBER: 60/056,845
17	EARLIER FILING DATE: 1997-08-22
18	EARLIER APPLICATION NUMBER: 60/056,892
19	EARLIER FILING DATE: 1997-08-22
20	EARLIER APPLICATION NUMBER: 60/057,761
21	EARLIER FILING DATE: 1997-08-22
22	EARLIER APPLICATION NUMBER: 60/047,595
23	EARLIER FILING DATE: 1997-05-23
24	EARLIER APPLICATION NUMBER: 60/047,599
25	EARLIER FILING DATE: 1997-05-23
26	EARLIER APPLICATION NUMBER: 60/047,588
27	EARLIER FILING DATE: 1997-05-23
28	EARLIER APPLICATION NUMBER: 60/047,585
29	EARLIER FILING DATE: 1997-05-23
30	EARLIER APPLICATION NUMBER: 60/047,586
31	EARLIER FILING DATE: 1997-05-23
32	EARLIER APPLICATION NUMBER: 60/047,590
33	EARLIER FILING DATE: 1997-05-23
34	EARLIER APPLICATION NUMBER: 60/047,594
35	EARLIER FILING DATE: 1997-05-23
36	EARLIER APPLICATION NUMBER: 60/047,589
37	EARLIER FILING DATE: 1997-05-23
38	EARLIER APPLICATION NUMBER: 60/047,593
39	EARLIER FILING DATE: 1997-05-23
40	EARLIER APPLICATION NUMBER: 60/047,614
41	EARLIER FILING DATE: 1997-05-23
42	EARLIER APPLICATION NUMBER: 60/043,578
43	EARLIER FILING DATE: 1997-04-11
44	EARLIER APPLICATION NUMBER: 60/043,576
45	EARLIER FILING DATE: 1997-04-11
46	EARLIER APPLICATION NUMBER: 60/047,501
47	EARLIER FILING DATE: 1997-05-23
48	EARLIER APPLICATION NUMBER: 60/043,670
49	EARLIER FILING DATE: 1997-04-11
50	EARLIER APPLICATION NUMBER: 60/056,632
51	EARLIER FILING DATE: 1997-08-22
52	EARLIER APPLICATION NUMBER: 60/056,664
53	EARLIER FILING DATE: 1997-08-22
54	EARLIER APPLICATION NUMBER: 60/056,876
55	EARLIER FILING DATE: 1997-08-22
56	EARLIER APPLICATION NUMBER: 60/056,881
57	EARLIER FILING DATE: 1997-08-22
58	EARLIER APPLICATION NUMBER: 60/056,909
59	EARLIER FILING DATE: 1997-08-22
60	EARLIER APPLICATION NUMBER: 60/056,875
61	EARLIER FILING DATE: 1997-08-22
62	EARLIER APPLICATION NUMBER: 60/056,862
63	EARLIER FILING DATE: 1997-08-22
64	EARLIER APPLICATION NUMBER: 60/056,887
65	EARLIER FILING DATE: 1997-08-22
66	EARLIER APPLICATION NUMBER: 60/056,908
67	EARLIER FILING DATE: 1997-08-22
68	EARLIER APPLICATION NUMBER: 60/048,964
69	EARLIER FILING DATE: 1997-06-06
70	EARLIER APPLICATION NUMBER: 60/057,650
71	EARLIER FILING DATE: 1997-09-05
72	EARLIER APPLICATION NUMBER: 60/056,884
73	EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      61.1%; Score 1789; DB 4; Length 383;
Best Local Similarity 92.4%; Pred. No. 9.9e-175;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 NAVGQIMTFGSPVIGCGFISGNLVSVCVEYLLWKVYQKTPALAVKAGLKEEBTELKOL 249
DB 1 NAVGQIMTFGSPVIGCGFISGNLVSVCVEYLLWKVYQKTPALAVKAGLKEEBTELKOL 60
QY 250 NLHKTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRFDGWVSYNQPVFL 309
DB 61 NLHKTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRFDGWVSYNQPVFL 120
QY 310 AGMGLAFYMTVLGPDCTTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRKCGL 369
DB 121 AGMGLAFYMTVLGPDCTTGYAYTQGLSGFHPQVFDGSI SYNWNNGCSFYLATSKWVF 180
QY 370 VETGLISGLAQLSCILCVISVFMFGSPDLVSVPFEDIRSRFQGESITPTKIPETITE 429
DB 181 GSAGLISGLAQLSCILCVISVFMFGSPDLVSVPFEDIRSRFQGESITPTKIPETITE 240
QY 430 IYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIRESER 489
DB 241 IYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIRESER 300
QY 490 GIINGVQNSMNYLLDLHFIHIVILAPNPEAGLLVLSVSVFVAMGHIMYFPAQNTLGNK 549
DB 301 GIINGVQNSMNYLLDLHFIHIVILAPNPEAGLLVLSVSVFVAMGHIMYFPAQNTLGNK 360
QY 550 LFACGPDKEVKEKQNTSVV 571
DB 361 LFACGPDKEVKEKQNTSVV 382

RESULT 2
US-09-540-236-2490
; Sequence 2490, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2490
; LENGTH: 591
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2490

Query Match      4.6%; Score 136; DB 4; Length 591;
Best Local Similarity 19.2%; Pred. No. 6.3e-05;
Matches 120; Conservative 94; Mismatches 228; Indels 182; Gaps 27;

QY 18 ADVLTSAXFLLYLGHSLTSWGDGMWHFVAVSVFLV----- 51
DB 52 ADMVSAASISWAG-MLANGG-----YASAYLMGTGTFVLLALLAPYLRKFGKFTVP 105
QY 52 -----ELYNSLLLTAVYGLVAGSVLVGLGAIIGDWDKARLV-AQTSLVQVNVSVIL 105
DB 106 DTGDRFYKTAFLVAVVCLILACTTYVIGQMTGAGVAFSREFLEVDNSTGLIIAIVLVF 165
QY 106 CGTILMM-----VFLHKHELLTVMHGVLTSCYILITIAN-----IANLASTATAITQ 155
DB 166 YAVLGNKGIITTVQAQYCVLMVAVIIPAFISLNTGNPIFQIGMFGNDVSTGMPILOK 225

156 RDWVWVAGEDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFI----- 208
226 LDMVLADLG-----FAQYTDVDP--NKLNMFLTNLSL-MIGTAGLPHVIRFTVVKVSD 277
209 -----SCWNLVSMCVVEYLLWKVYQKTPALAVKAGLKEEBET-----ELKQLNLHKDTEP--- 257
278 ARISAGMTLIFIAL-----LYTTAPAVGSMWARLNINIVYPOGLNQPALAYEARPEWM 330
258 KPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRFDGWVSYNQPVFLAGMGLAFL 317
331 KWWTETGLLYKEDKN-----NDGLIQYNDK----- 356
318 YMTVLGDFDCTTGYAYT-----OGLSGSILS-----ILMGASAITGIMGTVAFTWLRKCG 368
357 -----NEEYATVTAEBKWOGNELTANNDILVLANPEIANLP-----SWV---IG 398
369 LVRTGLISGLAQLSCILCVISVFMFGSPDLVSVPFEDIRSRFQGESITPTKIPETITE 428
399 LIAAGGLAALSTAAGLLLAISAISHDLIKTKIP--DINDK---GELMAARISMTIAI 453
429 EYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVI 485
454 VVATYLGMPNPPGFTAQWAVAFGIAASSLFPALMMGIFSKRI-----NST 498
486 ESERGIINGVQNSMNYLLDLHFIHIVILAP-----NPEAFGLLVLSVSVFVAMGHIMYF 539
499 GATAGMIAGLSATCTIVFLYMGWFFI---PGTNSFKNVEANWILGVSPUSFGAIGAVINP 555
540 --RFAQNTLGNKLPACGPDKEVR 561
556 IVAIAVSAMGN-----PPPKEVQ 573

RESULT 3
US-08-928-692-12
; Sequence 12, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Iaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 amino acids
; TYPE: amino acid
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; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13226
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13226

Query Match      4.0%; Score 117; DB 4; Length 490;
Best Local Similarity 18.5%; Pred. No. 0.0042;
Matches 95; Conservative 62; Mismatches 136; Indels 218; Gaps 25;

QY 3 RAGDNRQCGCGSLADYLTSAKFLLYLGHLSLSTWGDWYHFAVSVELVELY-----54
DB 9 RADEN-----CCDSLL-----ISIEGTTMQ--AIISEFTEIFSQPAFLMG 47

QY 55 -----GNSLL-----LTAVVGLVVA-----GSVLVLGAIGDWD 84
DB 48 LIAFVGLVALRSPGNKLLTGTLKPILGYLMSAGAGVIVANLPGLGIIIEAGNIRGVP 107

QY 85 KN-ARLKVQAQTSLVQNVSVILCGIILMMVFL-----HGHELLTWYHGWLTSCVILITI 139
DB 108 NNEAIVSAQKMLGVETMSILLGFIPLNLIARCTKYKFIPLTGHSHSFFLACLESAYLQA 167

QY 140 ANIANLASTATAITIQDRIWVWVAGEDRSKLANNNATIRIDQLTNIIAPMAVQIMTFG 199
DB 168 AEF-----QWMLLILIG-----179

QY 200 SPVIGCGFISG-WNLVSMCVEXVLLMKVYKTPALAVKAGLKBETELKQNLNKHDTPEK 258
DB 180 -----GELLGWSAIS-----PAIG-----QRYTRQVTE-- 203

QY 259 PLEGTHLMGVKDSNIHELEHBOEPTCASQMAEPFTRPDGMVS-----YINQPVLAGMGL 314
DB 204 --DG-----GIAMHFGSGJYVLSAWIARSTGNPANSFADTSEISKWGLRDTTWTG-- 254

QY 315 APLVMTVLGFDG-ITGYAYTOGLSGS-----ILSILMGASAITGIMGTVAFTWLRKCGLV 370
DB 255 --IVMFVIYFVCSAVAGSAYLSTIDQNLIFSVLTGLQFAVG--AIVYANGVR-----304

QY 371 RTGLISGLAQLSCILCVISVMPGSPDLVSPEDIRSRFIQESITPKIETITEI 430
DB 305 ---LILG-----DL-VPAFGISQKLI-----PDSIPAVDCAV 333

QY 431 YMSGNSGANIVETSPRSVPITISVLLPAGVI 463
DB 334 FFT-----FSPITAVVGVFISSFVGGLV 355

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RESULT 6
US-09-489-039A-14206
; Sequence 14206, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14206
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14206

Query Match      3.9%; Score 113.5; DB 4; Length 329;
Best Local Similarity 20.1%; Pred. No. 0.005;
Matches 78; Conservative 55; Mismatches 133; Indels 123; Gaps 15;

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QY 45 AVSVFLVELYGNLSLLLTAVYGLVWAGSVLVLCALIGDWVDMKARLKVACTSLVQNVSVI 104
DB 25 AMTAFELQQLINGLTGLGAVYGLAIGYTMVYG-IIG-----MINFAHGE--VTWVSAY 74

QY 105 LC--GIILMMVF-LHKHELL-----TWYHGWLTSCVILITIITIANLASTAT 150
DB 75 LCAIGLALLSFFGIHSPFLIIATLVFTIVTVGVYGAIER--IAYRPLENSTRPLAPLS 132

QY 151 AI---TIQDRIWVWAGEDRSKLANNNATIRIDQLTNIIAPMAVQIMTFGSPVIGCOF 207
DB 133 AIGMSLILQNVYQLSQPNQOQIPTLLSGALR-----MTVGDGVYQIITW 176

QY 208 ISGNLVSMCVEXVLLMKVYKTPALAVKAGLKBETELKQNLNKHDTPEKLEGTHLMG 267
DB 177 TKVFIILVAALVGLMLITWIIQYTRIGRICRAIQQR-----RVAAILG 219

QY 268 VKDSNIHELEHEQEPTCASQMAEPFTRPDGMVSYYNQPVFLAGMGLAFLYMTVLGFDGI 327
DB 220 INTDRVISL-----VFVIGAMAGLAGVL-----V 244

QY 328 TTGYAYTOGLSGSILSILMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQ-----380
DB 245 TMNYGTDFYIGFIIGIKAFATAVLGGIGSLP-----GAMUGLGLLVGAEOAFAGLV 296

QY 381 -----LSCLILCVISVEMP-----GSPL 398
DB 297 NSDYKDVFSFALLVAILIFRPQGLLGRPL 325

RESULT 7
US-09-252-991A-33032
; Sequence 33032, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33032
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33032

Query Match      3.8%; Score 112; DB 4; Length 305;
Best Local Similarity 18.3%; Pred. No. 0.0063;
Matches 71; Conservative 65; Mismatches 112; Indels 140; Gaps 16;

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QY 48 VFLVELYGNLSLLLTAVYGLVWAGSVLVLCALIGDWVDMKARLKVACTSLV-----97
DB 5 IFTQQMI-NGLTGLSVYGLAIGYTMVYGIIGNINFAHGEVYMWISAYLSAIALALLAFPG 63

QY 98 VQNVSVILCGIILMMVFLHKKHELLTWYHGWLTSCVILITIITIANLASTATAI---TI 154
DB 64 LQNFPLILITGLITFTV-----LVTCYGNVIER--IAYKPLENSTRPLAPLSAIGMSLI 115

QY 155 QRDWVWVWAGEDRSKLANNNATIRIDQLTNIIAPMAVQIMTFGSPVIGCGFIS-----209
DB 116 LQNVVQAQGPQQGI-----PTLDDGALKFH---VGDGFEVQLTYTK 154

QY 210 -----GWNLVSMCVEXVLLMKVYKTPALAVKAGLKBETELKQNLNKHDTPEKPL 260
DB 155 LFILIASLIGNAVITYVIRTKLGRCAI-----QQDRKM-----190

QY 261 EGTLMGVKDSNIHELEHBOEPTCASQMAEPFTRPDGMVSYYNQPVFLAGMGLAFLYMT 320

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Db 191 --ASILGINTDRV-----ISY-----VFVIGAAVAALAGV 218  
QY 321 VLGFDCITTYAVTQGLSGSILMSGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQ 380  
Db 219 L-----ITWNYGTFYAGFIGIKAFPAVGLGGISLP-----GAMLGGLVLGVAE 265  
QY 381 -----JSCLLICVSVFMP 394  
Db 266 AOFSGMVTYKDVFAFSLVLLILIFRP 293

RESULT 8  
US-09-328-352-4392  
; Sequence 4392, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4392  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4392

Query Match 3.8%; Score 110; DB 4; Length 429;  
Best Local Similarity 19.8%; Pred. No. 0.018;  
Matches 91; Conservative 78; Mismatches 158; Indels 132; Gaps 23;  
QY 20 YLTSAKELLY--LGHS---LSTGDRMWHFAVSFLVELYGNLSLLTA----- 62  
Db 4 YDIIRIYFNDLSHSYNFLMTMTTSHQFSQSLIYM-LIGSAILALSLGVRHGFGLYL 62  
QY 63 -----VYGLVAGSVVLGAI---IGDWDRKVARLKVAQTSLLVQNVSVILCG 107  
Db 63 VPMSEHFGHGVHVSIAAMQNLINGAIOPTGATADKYG-----SKVVVTVGGLLYT 115  
QY 108 I-ILMVFLHKHLLTMVHGWLTSYILITITIANIANLASTAITTORDMIVVWAGED 166  
Db 116 LGULLMAF-----SSSVLILNLSGLIIGALSATSFTVLLSAVGRAPPE 161  
QY 167 RSKLANMATIRIDQLTNILAPMAVGQIMTFGSPVCGGHSIGNW-----LVSMCV 218  
Db 162 KSMANGIAS-----AAGSGFGFMPLPSTLLLLKTV-GWSSALMVSAALLIALII 209  
QY 219 EYVLLKVVYQKTPALAVKAGLKEETELKQLNLHKDTEPKP-----LEG 262  
Db 210 P-LAWML--KGPSNQTPKAIAQPLTKQV-LHIARKHKPFWWLALGFLVCGFQVVFLG 264  
QY 263 THLMGVKDSNIHELHEQEPTCAS-----QMAEPTPTFGWV-SYVQVFLAGM--- 312  
Db 265 VHLPG-----YLIHGHEDATTGTFLALVGFNIVTYGAGWLGDRFSKPKLLMALYGS 318  
QY 313 -GLAFLYMTVLGFDCTTGYAY-----TQGLSGSILSILMGASAITGIMGTVAFT 361  
Db 319 RGIAIIAFLLLPLSTYTV-YAFGIIMGLLMLSTVPLTNGIVANMEGVKYLMSLSIVFFT 377  
QY 362 WLRKCGLVRTGLISGL-----AQUSCLILCVISVFMFG 395  
Db 378 ---HQVGSFFGWLGVGNHDLTGNYNAINLWLCIALSILG 413

RESULT 9  
US-09-134-001C-4610  
; Sequence 4610, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4610  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4610

Query Match 3.7%; Score 109.5; DB 4; Length 470;  
Best Local Similarity 19.5%; Pred. No. 0.023;  
Matches 100; Conservative 85; Mismatches 190; Indels 137; Gaps 21;  
QY 73 LVLGAIIGDWD-----KNARKKVAQTSLVQNVSVILCGIILMMVFL 115  
Db 45 LILGTIFLDAYDITILGNTDQTOQFHLSPATLSIVMTSLFIFGALFGALGGTLAYQFG 104  
QY 116 HKHELLTMVHGWLTSYILITIANI-ANLASTATAITIQDWTIVVWAGEDR----- 167  
Db 105 RKR-----ILSIALLTITVSLGAALAPNVILLICRCINGPAIGMDSPVAFTFI 154  
QY 168 SKLANMATIRID--QLTNILAPMAVGQIMTFGSPVCGG-----FISGMNLVSMCV 220  
Db 155 AETSNLKHKGRNVVQVWVYVAIVTSALAVT-AFFMLGAGAHLRVAVGFGALIAFVLY 213  
QY 221 VLLKVVYQKTPALAVKAGLKEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQ 280  
Db 214 ILIRKVLHSPSTVWVNHYSLEXATEFIRKYHKD-----IHLEGLEDDLN----- 259  
QY 281 EPTCASQMAEPTPTRDGWMVSYVNPFLA-----GMGLAFLYMTVLGFDCT 328  
Db 260 ----SDVTSPHNSWTDLEKPYIKRIILATAISTLQGMQVYGVG---LYIPIIA----- 306  
QY 329 TGVAYTQGLSGSILSILMGASA--ITGIMGTVAFTWLRKCGLVRTGLISGLAQSLIL 386  
Db 307 ----TYLISKDKIGVLLGTAVINAGILGAYLGAQLTKLGTTRKLTMI-GFTLLVLSMV 360  
QY 387 CVISVFMGSPDLDSVPEDIRSFIOGESITP-TKIPEITTEIYMGNSGNSANIVPET 445  
Db 361 CV-GLFYHHLPLMLNTF---LIGLFLGHSGGPGTGKTCIGALSFPPTHLRSQATGFVES 415  
QY 446 SPESVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIESERGIINGVQNSMYLLDL 505  
Db 416 VERTGSIIGTFVF--PIILAAVGLTN----- 439  
QY 506 LHPFIVILAPNPEAFGLLVLSVSVFAMG-HI 536  
Db 440 ---TMLLSIVP-LLGIIITVSIKWEAVGKHI 467

RESULT 10  
US-08-118-270-19  
; Sequence 19, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004



Db 108 -----SLLAGLSDIRNITIAFVRLPELVQGLITFGSAAY-LAWLSGKMM 152  
Qy 211 -----WNLVSMCEVYVLLMKVYQKTPALAVKAGLKEETEL-----KQNLHKD 254  
Db 153 LVTALMALTWGGFVLVSRVYKH-----MASLRETEKLYHDYQTVLEGRKELTLNRE 206  
Qy 255 TEKPELEGTHLMGVKDSNIHELEHEQEPCTCASQMAEPERTFRDGMVSYNQPVFLAGWGL 314  
Db 207 RBYVFNQYLDAREYRHIVR-----ADTFHLSAVNW-----SNIMLGAIGL 251  
Qy 315 AFLYMTVLGDFCITTYGAYVTOGLSGSILSMGASAITGIMGTVAFTWLRKRCGLVRTGL 374  
Db 252 VFWMANSLGW-----ADTAVAAVTSLTLL-----FLRPTL 281  
Qy 375 ISGLAQLSCLI 385  
Db 282 LSAVGALPTLL 292

## RESULT 13

US-08-595-553A-2

; Sequence 2, Application US/08595553A

; Patent No. 6391579

; GENERAL INFORMATION:

; APPLICANT: NANCY CARRASCO, ET AL.

; TITLE OF INVENTION: THYROID SODIUM/IODIDE SYMPORTER AND

; TITLE OF INVENTION: NUCLEIC ACID ENCODING SAME

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: AMSTER, ROTHSTEIN &amp; EBENSTEIN

; STREET: 90 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE

; MEDIUM TYPE: DISKETTE

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,553A

; FILING DATE: FEBRUARY 1, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CRAIG J. ARNOLD

; REGISTRATION NUMBER: 34,287

; REFERENCE/DOCKET NUMBER: 96700/393

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 697-5995

; TELEFAX: (212) 286-0854 or 286-0082

; TELEFAX: TWX 710-581-4766

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 618

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; DESCRIPTION: PROTEIN

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; INDIVIDUAL: RAT

; INDIVIDUAL ISOLATE: SODIUM/IODIDE SYMPORTER

US-08-595-553A-2

Query Match 3.7%; Score 108; DB 4; Length 618;

Best Local Similarity 19.1%; Pred. No. 0.051;

Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;

Qy 14 CGSLADYLTSAKFLLYGLHSLTWGDRMWHFAVSVFLVELYGNLSLLLTAVYGLVAGSVL 73

Db 132 CGTL-QYLVAT--MLYTG-----IVYAPALILNQVTGLDIWASLL 169

Qy 74 VLGAIGDWDKNAKLVKAQTSIVYQNVSVILCGIILMMVFLHKHELLTMYHGWV-LTSC 132  
Db 170 STGIICLTLYTGGMKAVVWTD--VPQVVVMLVGF-----WILARG 209  
Qy 133 YILIIITIANIANLATAITTIQ-----RDMIVVVAG-----164  
Db 210 VILGGPRNVLSLAQNHRSINLMDPDPDRSRYTFTWTFIVGGTLVWLSMGVYQNAQVORY 269  
Qy 165 -----EDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFTSGWNLVSMCWE 219  
Db 270 VACHTEGKAKALL-----VNQL-----GULIVASAC-CG-----300  
Qy 220 YVLLMWVYQK--TPALAVKAGLKEETELKQNLHKDTEPKP-----LEGTH 264  
Db 301 --IVMFVYVYKDCDPLLTGTSAPDQWMLLVLDIFEDLPVGLFLACAYSGTFLSTASTS 358  
Qy 265 LMGVKDSNIHELEHEQEPCTCASQMAEPFRTRFDGWSYVYNQPVFLAGMGLAFYMTVLGF 324  
Db 359 INAMAATVEDLIKPRMPGLAPR-----KLVFIS-KGLSFIY---GS 396  
Qy 325 DCITTCYAVTQGLSGSILSMGASAITG---IMGTV-----APT--WLRKCGI---VR 371  
Db 397 ACTLV-----AALSSLLGGVQLGSGFTVMGVISGPLLGAFTLGMLLPACNTPGVL 446  
Qy 372 TGLISGLAQLSCLILCVISVFMVPGSPDLDSVSPFFEDIRSRFTQGBSITPKIPEITTEIY 431  
Db 447 SGLAAGLA-VSLWVAVGATLYPPGE-----CTMGVLP TSAAGCTNDSV 488  
Qy 432 M---SNGSNSANIVPETSPE-----SVFIIISVLLFAGVIAARIGLWNSFDTLVTQLL 480  
Db 489 LLGPPGATNASGIPSSGMDTGRPALADTFYALSILYIYGALG-----TLTML 536

## RESULT 14

US-09-640-198D-4

; Sequence 4, Application US/09640198D

; Patent No. 6586411

; GENERAL INFORMATION:

; APPLICANT: Russell, Stephen

; APPLICANT: Kay Whye, Peng

; TITLE OF INVENTION: System for Monitoring the Location of

; TITLE OF INVENTION: Transgenes

; FILE REFERENCE: 07039-295001

; CURRENT APPLICATION NUMBER: US/09/640,198D

; CURRENT FILING DATE: 2000-08-16

; PRIOR FILING DATE: 1999-08-16

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 618

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-640-198D-4

Query Match 3.7%; Score 108; DB 4; Length 618;

Best Local Similarity 19.1%; Pred. No. 0.051;

Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;

Qy 14 CGSLADYLTSAKFLLYGLHSLTWGDRMWHFAVSVFLVELYGNLSLLLTAVYGLVAGSVL 73

Db 132 CGTL-QYLVAT--MLYTG-----IVYAPALILNQVTGLDIWASLL 169

Qy 74 VLGAIGDWDKNAKLVKAQTSIVYQNVSVILCGIILMMVFLHKHELLTMYHGWV-LTSC 132

Db 170 STGIICLTLYTGGMKAVVWTD--VPQVVVMLVGF-----WILARG 209

Qy 133 YILIIITIANIANLATAITTIQ-----RDMIVVVAG-----164

Db 210 VILGGPRNVLSLAQNHRSINLMDPDPDRSRYTFTWTFIVGGTLVWLSMGVYQNAQVORY 269

Qy 165 -----EDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFTSGWNLVSMCWE 219



Db 270 VACHTEGAKUALL-----VNQL-----GLFLIVASAAC-CG----- 300  
QY 220 YVLLKVKYQK--TPALAVKAGLKEEBETELKQINLHKDTEPKP-----LEGTH 264  
Db 301 --IVMFVYKDCDPLTGRISAPDQYMPLLVDIFEDLPVPGFLACAYSGTLSTASTS 358  
QY 265 LMGVSDNIHELEHTEOETCASQMAEPRTFRDQWVSYNQVFLAGMGLAFIYMTVLGF 324  
Db 359 INAAAVTEDLIKPRMFLAPR-----KLVFIS-KGLSFIY-----GS 396  
QY 325 DCITTYGAYTQGLSGSILSLMGASAITG---IMGTV-----AFT--WLRKQGL--VR 371  
Db 397 AGLTV-----AALSSLLGGVLOGSFTVMGVISGPLLGAFTLGMILLPACNTPCVL 445  
QY 372 TGLISGLAQLSCLILCVISVFMWPGSPDLVSPPEDIRSRFQGESITPTKIPITTEIY 431  
Db 447 SGLAAGLA-VSLWAVAGATLYPPGE-----QTMGVLFPSAAGCTNDVS 488  
QY 432 M---SNGSNSANIVPETSPE-----SVPIISVSLLEFAGVIAARIGLWSFDLTVTQLL 480  
Db 489 LLGPFPGATNASNGIFSSGMDTGRPALADTFIAISLYLYGALG-----TLTWM 536

RESULT 15  
US-09-543-681A-8251  
; Sequence 8251, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 8251  
; LENGTH: 491  
; TYPE: PRN  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-8251

Query Match 3.7%; Score 107.5; DB 4; Length 491;  
Best Local Similarity 19.7%; Pred. No. 0.039;  
Matches 102; Conservative 68; Mismatches 152; Indels 197; Gaps 27;

QY 29 YLGHSLSTWGRMWHFA-----VSVELVELYGN-----LLLTAVYGLVWAGS----- 71  
Db 28 YLIFSIELW-ERFGYGLQGIMAVYLVKMLGNSEAEAITVFAAFTALYGFVAIGWGLGD 86  
QY 72 -----VLVLGAIIGDWVDKNAKLVACTSLVQNVSVILCGII----- 109  
Db 87 KILGTRVIVLGAIV-----LAIGYAMVAFSCHDKDVIYWGGLATIAVGNGLFKANPSS 139  
QY 110 LMMVFLHKHE-----LLTWY-----HGWWLT--SCYILITIA 140  
Db 140 LLATCYEKDDPOLDGAFTMYMYSINVGSLMLATPWLAAANYGMDVAFALSVVGNMLITLA 199  
QY 141 NIANLASATATITORDMIVVAGVDRSKLANMNAT--IRRIDQLTNILAPMAV----- 192  
Db 200 N-----FMLCRGMI-----KDKSRDPFEPFLNYLKULLLVGIVALTAVSTWLLH 244  
QY 193 -QQIMTFGSPVIGCGFISGWNIV-----SMCEYEVLLMKYQKTP 231  
Db 245 NNEVATWSLAIISLGII-----LIFARETFMMKGVARRKMWIVAFLLWVEAVVFFVLYDQMP 300  
QY 232 ALAVKAGLKEEBETELKQINLHKDTEPKPLEGTHLGVKDSNIHELEH-----EQEPTCAS 286  
Db 301 T-----SINFFA-----IHNVEHAILGFSVEP----- 322  
QY 287 QMAEPRTFRDQWVSYNQVFLAGMGLAFIYMTVLGFDCTTGYAYTQG--LSGSILSI 344

Db 323 ----EQFQSLNPFW-----IMLASPLLAAY-NFMG-DKLPMPYKFTVGMFLSATAFLV 370  
QY 345 LMGASAITGIMGTVAFTWLRKQGLVRTG--LIS--GLAQLSCLILCVISVFMWPGSPDL 400  
Db 371 LPLGASMANEAGIVSSWMLVASYGFQSIGELMISGLGLAMVAQLVFORLMTGFMGAFLT 430  
QY 401 SVSPFEDIRSRFQGESITPTKIPE-----ITTEIYMS 433  
Db 431 SAA-----AAITAGKVASLMAVPEVDQNAHASLEIYSS 463

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Job time : 21 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2004, 18:04:06 ; Search time 50 Seconds  
(without alignment)  
3585.048 Million cell updates/sec

Title: US-09-715-927-6  
Perfect score: 2929  
Sequence: 1 MTRAGDHNRQCCGSLADY.....ACGPDKEVKENQANTSVV 571

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2929	100.0	571	15 US-10-341-434-169	Sequence 169, App
2	2929	100.0	571	15 US-10-331-496A-32	Sequence 32, Appl
3	2925	99.9	571	12 US-10/399	Sequence 2, Appli
4	2924	99.8	571	10 US-09-973-180-2	Sequence 2, Appli
5	2924	99.8	571	10 US-09-973-180-3	Sequence 3, Appli
6	2922	99.8	571	10 US-09-973-180-4	Sequence 4, Appli
7	2917	99.6	571	9 US-09-729-674-130	Sequence 130, App
8	2018	68.9	408	15 US-10-264-049-3007	Sequence 3007, Ap
9	1789	61.1	382	15 US-10-264-237-1491	Sequence 1491, Ap
10	1789	61.1	383	10 US-09-809-391-460	Sequence 460, App
11	1789	61.1	383	10 US-09-882-171-460	Sequence 460, App
12	1789	61.1	383	12 US-10-164-861-460	Sequence 460, App
13	656	22.4	484	16 US-10-437-963-157454	Sequence 157454,
14	605	20.7	511	12 US-10-425-114-67781	Sequence 67781, A
15	329	11.2	597	12 US-10-425-114-67278	Sequence 67278, A

16	318.5	10.9	552	16	US-10-437-963-134922	Sequence 134922,
17	285	9.7	587	12	US-10-424-599-195397	Sequence 195397,
18	271.5	9.3	593	16	US-10-437-963-122654	Sequence 122654,
19	248	8.5	159	12	US-10-424-599-269044	Sequence 269044,
20	188.5	6.4	150	12	US-10-424-599-221969	Sequence 221969,
21	171	5.8	129	12	US-10-424-599-271491	Sequence 271491,
22	126.5	4.3	523	15	US-10-099-322-122	Sequence 122, App
23	126.5	4.3	523	15	US-10-044-564-122	Sequence 122, App
24	126	4.3	523	12	US-10-403-161-36	Sequence 36, Appl
25	125.5	4.3	575	14	US-10-156-761-10350	Sequence 10350, A
26	124.5	4.3	523	15	US-10-099-322-123	Sequence 123, App
27	124.5	4.3	523	15	US-10-044-564-123	Sequence 123, App
28	124	4.2	529	12	US-10-403-161-38	Sequence 38, Appl
29	123.5	4.2	487	12	US-10-403-161-44	Sequence 44, Appl
30	123.5	4.2	524	12	US-10-403-161-34	Sequence 34, Appl
31	123.5	4.2	524	12	US-10-403-161-40	Sequence 40, Appl
32	123.5	4.2	524	12	US-10-403-161-42	Sequence 42, Appl
33	123.5	4.2	524	15	US-10-099-322-34	Sequence 34, Appl
34	123.5	4.2	524	15	US-10-099-322-121	Sequence 121, App
35	123.5	4.2	524	15	US-10-044-564-34	Sequence 34, Appl
36	123.5	4.2	524	15	US-10-044-564-121	Sequence 121, App
37	120	4.1	458	14	US-10-283-423-6	Sequence 6, Appli
38	120	4.1	458	14	US-10-213-821-6	Sequence 6, Appli
39	120	4.1	458	16	US-10-736-048-6	Sequence 6, Appli
40	119	4.1	537	9	US-09-738-626-6730	Sequence 6730, Ap
41	118.5	4.0	522	15	US-10-099-322-124	Sequence 124, App
42	118.5	4.0	522	15	US-10-044-564-124	Sequence 124, App
43	117.5	4.0	494	15	US-10-369-493-12526	Sequence 12526, A
44	114.5	3.9	424	9	US-09-738-626-3641	Sequence 3641, Ap
45	114.5	3.9	424	12	US-10-627-476-600	Sequence 600, App

ALIGNMENTS

RESULT 1  
US-10-341-434-169  
; Sequence 169, Application US/10341434  
; Publication No. US20030215835A1  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes  
; FILE REFERENCE: 9U 204 205 R1  
; CURRENT APPLICATION NUMBER: US/10/341,434  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/348,164  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/348,119  
; PRIOR FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 169  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-341-434-169

Query Match	100.0%;	Score	2929;	DB	15;	Length	571;
Best Local Similarity	100.0%;	Pred. No.	1.7e-272;				
Matches	571;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MTRAGDHNRQCCGSLADYLTSAKFLLYLGHSLSTWGD	RMHFAVSFVLVELYGN	SLLL	60		
Db	1	MTRAGDHNRQCCGSLADYLTSAKFLLYLGHSLSTWGD	RMHFAVSFVLVELYGN	SLLL	60		
Qy	61	TAVYGLVAGSVLVGAIIGDWDKNAKLVQTSVQVNVSVIL	CGIIMVFLKH	HEL	120		
Db	61	TAVYGLVAGSVLVGAIIGDWDKNAKLVQTSVQVNVSVIL	CGIIMVFLKH	HEL	120		
Qy	121	LTMYHGVNLSVCSYLIITITIANIANLASTATAITIQRD	WIVVWAGEPSKLAN	NATIRI	180		
Db	121	LTMYHGVNLSVCSYLIITITIANIANLASTATAITIQRD	WIVVWAGEPSKLAN	NATIRI	180		

Qy	181	DQLTNLLAPMAVGQIMTFGSPVIGCGFISGWNVLVSMCVVEYVLLWKVYQKTPALAVKAGLK	240
Db	181	DQLTNLLAPMAVGQIMTFGSPVIGCGFISGWNVLVSMCVVEYVLLWKVYQKTPALAVKAGLK	240
Qy	241	EBEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEOEPTCASOMAE2PFRTPRDGMV	300
Db	241	EBEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEOEPTCASOMAE2PFRTPRDGMV	300
Qy	301	SYNQPVFLAGNGLAFLYKTVLGPDCITTGAYYQGLSGSILSLKNGASAITGIMGTVP	360
Db	301	SYNQPVFLAGNGLAFLYKTVLGPDCITTGAYYQGLSGSILSLKNGASAITGIMGTVP	360
Qy	361	TWLRRCGGLVRLTGLISGLAQLSCLTLCVISVFMGSPDLDSVSPFEDIRSRFIOGESITP	420
Db	361	TWLRRCGGLVRLTGLISGLAQLSCLTLCVISVFMGSPDLDSVSPFEDIRSRFIOGESITP	420
Qy	421	TKIPEITTBIIYNSNGSANSANIVPETSPE5PVIISVSLLPAGVTAARIGLWSFBLTVTQLL	480
Db	421	TKIPEITTBIIYNSNGSANSANIVPETSPE5PVIISVSLLPAGVTAARIGLWSFBLTVTQLL	480
Qy	481	QENVIESERGIINGVQNSVNYLLDLHLHPIMVLAPNPEAFGLLVLSVSFVAMGHIMYPR	540
Db	481	QENVIESERGIINGVQNSVNYLLDLHLHPIMVLAPNPEAFGLLVLSVSFVAMGHIMYPR	540
Qy	541	FAQNTLGNKLFACGPDPAKEVRKENQANTSVV	571
Db	541	FAQNTLGNKLFACGPDPAKEVRKENQANTSVV	571
RESULT 2			
US-10-331-496A-32			
; Sequence 32, Application US/10331496A			
; Publication No. US20030228305A1			
; GENERAL INFORMATION:			
; APPLICANT: FRANTZ, GRETCHEN			
; APPLICANT: HILLAN, KENNETH J.			
; APPLICANT: PHILLIPS, HEIDI S.			
; APPLICANT: POLAKIS, PAUL			
; APPLICANT: SMITH, VICTORIA			
; APPLICANT: SPENCER, SUSAN D.			
; APPLICANT: WILLIAMS, P. MICKEY			
; APPLICANT: WU, THOMAS D.			
; APPLICANT: ZHANG, ZEMIN			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
TITILE OF INVENTION: TREATMENT OF TUMOR			

Query Match	100.0%;	Score 2929;	DB 15;	Length 571;
Best Local Similarity	100.0%;	Pred. No. 1.7e-272;		
Matches 571;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTRAGDHNRRQCGCGSLADYLSAKELLYLGHSLSTWGDMMWHFAVSFLVELYGNLSLL	60	
DB	1	MTRAGDHNRRQCGCGSLADYLSAKELLYLGHSLSTWGDMMWHFAVSFLVELYGNLSLL	60	
QY	61	TAYVGLVAGSVLVLAGIIGDWWDKNARUKVAQTSLVQNVSVILCGIILMMVFLKHKL	120	
DB	61	TAYVGLVAGSVLVLAGIIGDWWDKNARUKVAQTSLVQNVSVILCGIILMMVFLKHKL	120	
QY	121	LTMWYHGWLTSCVILITITIANIANLASTATATIQRDWIVVWAGEDRSKLANNNATIRI	180	
DB	121	LTMWYHGWLTSCVILITITIANIANLASTATATIQRDWIVVWAGEDRSKLANNNATIRI	180	
QY	181	DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVYVLLWKVYQKTPALAVKAGLK	240	
DB	181	DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVYVLLWKVYQKTPALAVKAGLK	240	
QY	241	EEETELKQLNLKXDTPEKPLEGTHLMGVKXDSNIHELEHEQEPTCASQMAEPRTFRDGVV	300	
DB	241	EEETELKQLNLKXDTPEKPLEGTHLMGVKXDSNIHELEHEQEPTCASQMAEPRTFRDGVV	300	
QY	301	SYYNQPVFLAGMGLAFLYMTVLGFDCTITTYAYTQGLSGSILSLMGASAITGIMGTAF	360	
DB	301	SYYNQPVFLAGMGLAFLYMTVLGFDCTITTYAYTQGLSGSILSLMGASAITGIMGTAF	360	
QY	361	TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVPFDIRSRFIOGESITP	420	
DB	361	TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVPFDIRSRFIOGESITP	420	
QY	421	TKPIETITTELYMSGNSANIIVPETSPEVPIISVLSLLFAGVIAARIGLWSEDLVTQLL	480	
DB	421	TKPIETITTELYMSGNSANIIVPETSPEVPIISVLSLLFAGVIAARIGLWSEDLVTQLL	480	
QY	481	QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSFVAMGHIMYPR	540	
DB	481	QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSFVAMGHIMYPR	540	
QY	541	FAQNTLGNKLFACGPDPAKEVRKENQANTSVV	571	
DB	541	FAQNTLGNKLFACGPDPAKEVRKENQANTSVV	571	
RESULT 3				
US/10/399				
; Sequence 2, Application US/10399488				
; Publication No. US20040029147A1				
; GENERAL INFORMATION:				
; APPLICANT: Pietrangolo, Antonello				
; TITLE OF INVENTION: Mutations in the ferroportin 1 gene associated with hereditary				
; FILE REFERENCE: 9907-097-999				
; CURRENT APPLICATION NUMBER: US/10/399,488				
; CURRENT FILING DATE: 2003-04-16				
; PRIOR APPLICATION NUMBER: PCT/EP01/12018				
; PRIOR FILING DATE: 2001-10-17				
; PRIOR APPLICATION NUMBER: MI2000A002240				
; PRIOR FILING DATE: 2000-10-17				
; NUMBER OF SEQ ID NOS: 8				
; SOFTWARE: PatentIn version 3.2				
; SEQ ID NO 2				
; LENGTH: 571				
; TYPE: PRt				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: misc feature				
; LOCATION: (77)..(77)				
; OTHER INFORMATION: The 'Xaa' at location 77 is either Asp or Ala depending on the				
US/10/399,488-2				
Query Match	99.9%;	Score 2925;	DB 12;	Length 571;

Best Local Similarity 99.8%; Pred. No. 4.1e-272;  
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60  
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120  
Db 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180  
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

QY 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240  
Db 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240

QY 241 EESTELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEOEPTCASQMAEPFRTRFDGWV 300  
Db 241 EESTELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEOEPTCASQMAEPFRTRFDGWV 300

QY 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSILMGASAITGIMGVAF 360  
Db 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSILMGASAITGIMGVAF 360

QY 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420  
Db 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIIGLWSFDLTVTQLL 480  
Db 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIIGLWSFDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSNMVLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
Db 481 QENVIESERGIINGVQNSNMVLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDCAKEVRKENQANTSVV 571  
Db 541 FAQNTLGNKLFACGPDCAKEVRKENQANTSVV 571

RESULT 4  
US-09-973-180-2  
; Sequence 2, Application US/09973180  
; Publication No. US20030082553A1  
; GENERAL INFORMATION:  
; APPLICANT: Oestra, Ben Heutink, P Duijin, C.M.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS  
; FILE REFERENCE: 24594  
; CURRENT APPLICATION NUMBER: US/09/973,180  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 60/301,429  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 99.8%; Score 2924; DB 10; Length 571;  
Best Local Similarity 99.8%; Pred. No. 5.2e-272;  
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-09-973-180-2

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60  
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120  
Db 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120

Db 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180  
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

QY 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240  
Db 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240

QY 241 EESTELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEOEPTCASQMAEPFRTRFDGWV 300  
Db 241 EESTELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEOEPTCASQMAEPFRTRFDGWV 300

QY 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSILMGASAITGIMGVAF 360  
Db 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSILMGASAITGIMGVAF 360

QY 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420  
Db 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIIGLWSFDLTVTQLL 480  
Db 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIIGLWSFDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSNMVLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
Db 481 QENVIESERGIINGVQNSNMVLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDCAKEVRKENQANTSVV 571  
Db 541 FAQNTLGNKLFACGPDCAKEVRKENQANTSVV 571

RESULT 5  
US-09-973-180-3  
; Sequence 3, Application US/09973180  
; Publication No. US20030082553A1  
; GENERAL INFORMATION:  
; APPLICANT: Oestra, Ben Heutink, P Duijin, C.M.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS  
; FILE REFERENCE: 24584  
; CURRENT APPLICATION NUMBER: US/09/973,180  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 60/301,429  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 144  
; OTHER INFORMATION:  
US-09-973-180-3

Query Match 99.8%; Score 2924; DB 10; Length 571;  
Best Local Similarity 99.8%; Pred. No. 5.2e-272;  
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60  
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120  
Db 61 TAVYGLVAVGSLVILGAIIGDWVDKNAKLVKAQTSLVVQNSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

Db 121 LTMHGWLTSCVILITITANTAHLASTATAITORDWIVVAGBDRSKLANMATIRRI 180  
QY 181 DQLTNLLAPMAVGQINTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240  
Db 181 DQLTNLLAPMAVGQINTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240  
QY 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300  
Db 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300  
QY 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360  
Db 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360  
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMPSGLDLSVSPEDIRSRFIQESITP 420  
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMPSGLDLSVSPEDIRSRFIQESITP 420  
QY 421 TKIPEITTIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480  
Db 421 TKIPEITTIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480  
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571  
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571  
RESULT 6  
US-09-973-180-4  
; Sequence 4, Application US/09973180  
; Publication No. US200308253A1  
; GENERAL INFORMATION:  
; APPLICANT: Oestra, Ben Heutink, P Duijin, C.M.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS  
; FILE REFERENCE: 24584  
; CURRENT APPLICATION NUMBER: US/09/973,180  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 60/301,429  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; LOCATION: 144  
; OTHER INFORMATION: Xaa = any amino acid except Asp  
US-09-973-180-4

Query Match 99.8%; Score 2922; DB 10; Length 571;  
Best Local Similarity 99.8%; Pred. No. 8e-272;  
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRAGDHNQRCCGSLADYLSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60  
Db 1 MTRAGDHNQRCCGSLADYLSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60  
QY 61 TAVYGLVAGSVLVLGAIIGDWVDRKALKVAQTSLLVQNVSVILCGIILMWFVLRKHEL 120  
Db 61 TAVYGLVAGSVLVLGAIIGDWVDRKALKVAQTSLLVQNVSVILCGIILMWFVLRKHEL 120  
QY 121 LTMHGWLTSCVILITITANTAHLASTATAITORDWIVVAGBDRSKLANMATIRRI 180  
Db 121 LTMHGWLTSCVILITITANTAHLASTATAITORDWIVVAGBDRSKLANMATIRRI 180  
QY 181 DQLTNLLAPMAVGQINTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240

Db 181 DQLTNLLAPMAVGQINTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240  
QY 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300  
Db 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300  
QY 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360  
Db 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360  
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMPSGLDLSVSPEDIRSRFIQESITP 420  
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMPSGLDLSVSPEDIRSRFIQESITP 420  
QY 421 TKIPEITTIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480  
Db 421 TKIPEITTIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480  
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571  
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

## RESULT 7

US-09-729-674-130  
; Sequence 130, Application US/09729674  
; Patent No. US20010039335A1

; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steinhilber II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Pechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/09/729,674  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: UNSURE  
; LOCATION: (202)  
; NAME/KEY: UNSURE  
; LOCATION: (504)  
US-09-729-674-130

Query Match 99.6%; Score 2917; DB 9; Length 571;  
Best Local Similarity 99.6%; Pred. No. 2.4e-271;  
Matches 569; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRAGDHNQRCCGSLADYLSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60  
Db 1 MTRAGDHNQRCCGSLADYLSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60

QY 61 TAVYGLVWAGSVLVIGALIGDWDVKNARLKVAAQTSVLVQNVSVILCGIILMMVFLKHGL 120  
Db 61 TAVYGLVWAGSVLVIGALIGDWDVKNARLKVAAQTSVLVQNVSVILCGIILMMVFLKHGL 120  
QY 121 LTMVHGWLTSCVYIIITITIANIANTASTATITIQDMMIVVAGEDRSKLANMNTIRRI 180  
Db 121 LTMVHGWLTSCVYIIITITIANIANTASTATITIQDMMIVVAGEDRSKLANMNTIRRI 180  
QY 181 DQLTNIIAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAGLK 240  
Db 181 DQLTNIIAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAGLK 240  
QY 241 EEETELKQNLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGV 300  
Db 241 EEETELKQNLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGV 300  
QY 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYATQGLSGSILSLMGASAITGIMTVAF 360  
Db 301 SYYNQPVFLAGMGLAFLYMTVLGFCITITGYATQGLSGSILSLMGASAITGIMTVAF 360  
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420  
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420  
QY 421 TKIPETITEIYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTOLL 480  
Db 421 TKIPETITEIYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTOLL 480  
QY 481 QENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
Db 481 QENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540  
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571  
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

## RESULT 8

US-10-264-049-3007  
; Sequence 3007, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133PI  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 3007  
; LENGTH: 408  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-049-3007

Query Match 68.9%; Score 2018; DB 15; Length 408;  
Best Local Similarity 100.0%; Pred. No. 4.6e-185;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 RIDQLTNIIAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAG 238  
Db 16 RIDQLTNIIAPMAYGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAG 75  
QY 239 LKBEETELKQNLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDG 298  
Db 76 LKBEETELKQNLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDG 135  
QY 299 WSYYNQPVFLAGMGLAFLYMTVLGFCITITGYATQGLSGSILSLMGASAITGIMTV 358

Db 136 WSYYNQPVFLAGMGLAFLYMTVLGFCITITGYATQGLSGSILSLMGASAITGIMTV 195  
QY 359 AFTWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESI 418  
Db 196 AFTWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESI 255  
QY 419 TPKIPETITEIYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTVQ 478  
Db 256 TPKIPETITEIYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTVQ 315  
QY 479 LLENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMY 538  
Db 316 LLENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMY 375  
QY 539 FRPAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571  
Db 376 FRPAQNTLGNKLFACGPDPAKEVRKENQANTSVV 408  
RESULT 9  
US-10-264-237-1491  
; Sequence 1491, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133PI  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1491  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-237-1491  
Query Match 61.1%; Score 1789; DB 15; Length 382;  
Best Local Similarity 92.4%; Pred. No. 4.6e-163;  
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;  
QY 190 MANGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAGLKEETELKQ 249  
Db 1 MANGQIMTFGSPVIGCGFISGMNLVSMCVVEYVLLMKVYQKTPALAVKAGLKEETELKQ 60  
QY 250 NLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGVSYYNQPVFL 309  
Db 61 NLHKDTEPKLEGLTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGVSYYNQPVFL 120  
QY 310 AGMGLAFLYMTVLGFCITITGYATQGLSGSILSLMGASAITGIMTVAFWLKRCGL 369  
Db 121 AGMGLAFLYMTVLGFCITITGYATQGLSGFHPQYDFDGSISYNNNGNSFYLATSKMWF 180  
QY 370 VRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITPKIPETITE 429  
Db 181 GSAGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITPKIPETITE 240  
QY 430 IYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTVQQLQENVIESER 489  
Db 241 IYNSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTDTVQQLQENVIESER 300  
QY 490 GINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFRPAQNTLGNK 549  
Db 301 GINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFRPAQNTLGNK 360  
QY 550 LFACGPDPAKEVRKENQANTSVV 571  
Db 361 LFACGPDPAKEVRKENQANTSVV 382

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RESULT 10
US-09-809-391-460
; Sequence 460, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (383)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-460

Query Match          61.1%; Score 1789; DB 10; Length 383;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLMKVYQKTPALAVKAGLKEETELKQL 249
Db 1 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLMKVYQKTPALAVKAGLKEETELKQL 60
QY 250 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRTRFGDGVSYNQPVFL 309
Db 61 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRTRFGDGVSYNQPVFL 120
QY 310 AGMGLAFLVMTVLGFDCTTGTAYTQGLSGSILSMGASAITGIMGTVAFTLRRKQGL 369
Db 121 AGMGLAFLVMTVLGFDCTTGTAYTQGLSGSPFDGDSISVNNWNGCSFYLATSKWFF 180
QY 370 VRTGLISGLAQSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKPIPETTE 429
Db 181 GSAGLISGLAQSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKPIPETTE 240
QY 430 IYMSNGSNSANIVPETSPEVPIISVSLIFAGVIAARIGLMSFDLTVTLLQENVIESER 489
Db 241 IYMSNGSNSANIVPETSPEVPIISVSLIFAGVIAARIGLMSFDLTVTLLQENVIESER 300
QY 490 GIINGVQNSMNYLLDLHPIWILAPNPAFGLLLVLSVSPVAMGHIMYFRFAQNTLGK 549
Db 301 GIINGVQNSMNYLLDLHPIWILAPNPAFGLLLVLSVSPVAMGHIMYFRFAQNTLGK 360
QY 550 IFACGPDAAKEVRKENCNTSVV 571
Db 361 IFACGPDAAKEVRKENCNTSVV 382

RESULT 11
US-09-882-171-450
; Sequence 460, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
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; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
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;; PRIOR APPLICATION NUMBER: 60/043,669  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/043,312  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/043,313  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/043,672  
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;; PRIOR APPLICATION NUMBER: 60/043,315  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/048,974  
;; PRIOR FILING DATE: 1997-06-06  
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;; PRIOR APPLICATION NUMBER: 60/057,761  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/047,595  
;; PRIOR FILING DATE: 1997-05-23  
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;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,594

;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,589  
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;; PRIOR FILING DATE: 1997-05-23  
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;; PRIOR APPLICATION NUMBER: 60/056,876  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,881  
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;; PRIOR APPLICATION NUMBER: 60/056,862  
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;; PRIOR APPLICATION NUMBER: 60/056,887  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,908  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/048,964  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Query Match 61.1%; Score 1789; DB 10; Length 383;

Best Local Similarity 92.4%; Pred. No. 4.6e-163;  
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

Qy 190 MAVQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLKEEETELKQL 249  
Db 1 MAVQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYQKTPALAVKAGLKEEETELKQL 60  
Qy 250 NLHKDTEPKPLEGTHLMGVKDSNIHLEHEQEPTCASQVAEPPTFRDGVWSYINQPVFL 309  
Db 61 NLHKDTEPKPLEGTHLMGVKDSNIHLEHEQEPTCASQVAEPPTFRDGVWSYINQPVFL 120  
Qy 310 AGMGLAFYMTVLGDCITTTGYATQGLSGSILSLMGASAITGIMGTVAFTWLRKCGL 369  
Db 121 AGMGLAFYMTVLGDCITTTGYATQGLSGFHPQYEDGSISYNNNGNSFYLATSKMWF 180  
Qy 370 VRTGLISGLAQLSCLILCVISVEMPGSPDLDSVSPFEDRSRPIQGESITPTKIPITTE 429  
Db 181 GSAGLISGLAQLSCLILCVISVEMPGSPDLDSVSPFEDRSRPIQGESITPTKIPITTE 240  
Qy 430 IYMSNGSNSANIYPTSPSPVPIISVSLFAGVIAARIGLWSFDLTVTQLQSNVIESR 489  
Db 241 IYMSNGSNSANIYPTSPSPVPIISVSLFAGVIAARIGLWSFDLTVTQLQSNVIESR 300  
Qy 490 GINGVQNSNYLLDLLHFIWVILAPNEAFGLLVLSISFVAMGHIMYFRFAQNTLGNK 549  
Db 301 GINGVQNSNYLLDLLHFIWVILAPNEAFGLLVLSISFVAMGHIMYFRFAQNTLGNK 360  
Qy 550 LFACGPDKEVRKENQANTSVV 571  
Db 361 LFACGPDKEVRKENQANTSVV 382

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RESULT 12
US-10-164-861-460
; Sequence 460, Application US/10164861
; Publication No. US2003022548A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (383)
; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-460

Query Match      61.1%; Score 1789; DB 12; Length 383;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 MAVGQIMTSGSPVIGCGFISGNLVSMCVYVLLWKVYQKTPALAVKAGLKEEETELKQL 249
DB 1 MAVGQIMTSGSPVIGCGFISGNLVSMCVYVLLWKVYQKTPALAVKAGLKEEETELKQL 60

QY 250 NLHKTEPRLGTHLMGVKDSNIHELEHEQBPFCASQWAEFFRTFRDGTWYVYNQPVFL 309
DB 61 NLHKTEPRLGTHLMGVKDSNIHELEHEQBPFCASQWAEFFRTFRDGTWYVYNQPVFL 120

QY 310 AGMGLAFVMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGMGTVAFTWLRKCGL 369
DB 121 AGMGLAFVMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGMGTVAFTWLRKCGL 180

QY 370 VRTGLISGLAQLSCLILCVISVFMPSPLDLSVPFDIRSRFIQGESITPTKIPETITE 429
DB 181 GSAGLISGLAQLSCLILCVISVFMPSPLDLSVPFDIRSRFIQGESITPTKIPETITE 240

QY 430 IYMSNGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIRESER 489
DB 241 IYMSNGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIRESER 300

QY 490 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMYFPAQNTLGNK 549
DB 301 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMYFPAQNTLGNK 360

QY 550 LFACGPDKEVRKQNKQNTSVV 571
DB 361 LFACGPDKEVRKQNKQNTSVV 382

RESULT 13
US-10-437-963-157454
; Sequence 157454, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157454
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57023C.1.pap
US-10-437-963-157454

Query Match      22.4%; Score 656; DB 16; Length 484;
Best Local Similarity 29.9%; Pred. No. 6.8e-54;
Matches 157; Conservative 91; Mismatches 169; Indels 108; Gaps 8;

QY 28 LYLGHSLSTGDRMHFAVSVFLVELYGNLSLLLTAVYGLVAGSVLVGLAITGDWVDKNA 87
DB 27 LYVGHFLLARWARMWFEFVGLYIRIPGSLLLTAVYGVVEASAAALGPIYGAVDRLA 86

QY 88 RLKVAOTSLVQNVSVILQGIILMMVFLHKLHLLTWYHGWLTSCVILIITIANI---A 143
DB 87 YLOVLRLLWLLQGSFVAAGSVTALLVYGARLAA--GF---PAFVALVVVTVNSGALA 141

QY 144 NLASTATATTIORDWIVVVA--GEDRSKLANMATIRRIDQLNLIAPMAVGQIMTFSVPV 202
DB 142 ALSTLAGTILIEREMWVVIAGGQPAAVLTGINSVIRRIDLSCKLLAPVLSGFFISVSM 201

QY 203 ICGGFTISGNLVSMCVYVLLWKVYQKTPALAVKAGLKEEETELKQLNLHKDTEPKLEG 262
DB 202 ASAAALAAANLAAVWVQYVWLFVSVYAGFPAL-----SETQISRRADDDE---- 247

QY 263 THLMGVKDSNIHELEHEQBPFCASQWAEFFRTFR-----DGVSYNQVFLAGMG 313
DB 248 -----AAAAAQPKVERLMTMLPCWESWAVYARQEVVLPVGA 285

QY 314 LAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGMGTVAFTWLRKCGLVRTG 373
DB 286 LAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGMGTVAFTWLRKCGLVRTG 345

QY 374 LISGLAQLSCLILCVISVFMPSPLDLSVPFDIRSRFIQGESITPTKIPETITEIYMS 433
DB 346 LNSIWAQWCLLVCAVSWAGG----- 367

QY 434 NGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIRESERGIN 493
DB 368 -----AAPLASAMLMGGVAASRLGLMFPDLAVMQLMQDGPESDRCVVG 412

QY 494 GVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMY 538
DB 413 GVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMY 457

RESULT 14
US-10-425-114-67781
; Sequence 67781, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; SEQ ID NO 67781
; LENGTH: 511
; TYPE: PR
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3632-036-H10_FLI.pep
US-10-425-114-67781

Query Match      20.7%; Score 605; DB 12; Length 511;
Best Local Similarity 28.2%; Pred. No. 5.9e-49;
Matches 152; Conservative 103; Mismatches 186; Indels 98; Gaps 10;

QY 13 CGSLADYLTSKFL--LVLHSLSTWGRMHFAVSFLVELYGNLSLLLTAVYGLVAVAG 70
Db 40 CSGS---PLDAPILRLRYAGQILARWGEFVALYMKIRWIPDSLFLFAIYGVETS 96
QY 71 SVVLGAITGDVKNARLKVAQTSVLVQNVSVILCGIILMMVFLHKLHLLTMVHGWL 130
Db 97 SLVVLGPVVTLVGRATYQLVGLIWSQISLIVAGTAVTLLMYANLRATSF----- 150
QY 131 SCYILITITIANI-----ANLSTATAITTDRIWVWV-AGEBRSKLANNNATIRIDQLTN 185
Db 151 PAFMALVATNVSGAALASALAGTILIEREWVVISGHPSPSVRTGINSVYVRIDLGCS 210
QY 186 ILAPMAVGQIMTFGSPVIGCGPISGNLVSMCVBYVLLWKVYQKTPALAVRAGLKEETE 245
Db 211 LLAPVLSALVISLASTQASAAVLASTAASAGLQCLFVSVYNGVPALAAPQPRASDAE 270
QY 246 LKQNLHKTDEPKPLEGTHLMGVKDSNIHELEHEOEPTCA-----SMAEPRTFR--DGW 299
Db 271 -----RPPVPMT-----VAPAAEAPTQALDWARLADKLSVAGSWESW 309
QY 300 VSYNQPVPLAGMGLAFLYMTYVLGFDCTITGVAYTQGLSGSILSLMGASAITGIMGTVA 359
Db 310 VYARQDVALPGVALAFLYFTVLSFGTLMTATLWKGPAYVISIARGFSAIVIGATLL 369
QY 360 FTWLRKCKGLRIGTIGSLAQSLCILCVISVFMGSPDLDSVSPEDIRSRFIQGESIT 419
Db 370 YPLVHRSVSTLRTGLWSIMWQCLLCVASVW----- 402
QY 420 PKIPEITTEIYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLMSFDLTVTQL 479
Db 403 -----AATGVASAWMLMAGVAASRLGLWTFDLAVNQ 434
QY 480 LQENVIESRGIINGVQNSMYLLDLHFIWVILAPNEAFGLLLVLSVFMVGHIMY 538
Db 435 MODGVDPHERCVSVGVQNALQSVFDLLTVVAIVISDPKFSKMIVLFSFLVTCAAVNY 493

RESULT 15
US-10-425-114-67278
; Sequence 67278, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67278
; LENGTH: 597
; TYPE: PR
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4759-026-A6_FLI.pep
US-10-425-114-67278
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Query Match      11.2%; Score 329; DB 12; Length 597;
Best Local Similarity 22.9%; Pred. No. 2.7e-22;
Matches 125; Conservative 86; Mismatches 220; Indels 114; Gaps 14;

QY 26 FLAYLGHSLSTWGRMHFAVSFLVELYGNLSLLLTAVYGLVAVAGSVLVLGAITGDVVK 85
Db 145 YALYASYLFGNLVEQLWNFAWPATLALHPN--LLPVAIVGFFTKLSVFFGAPIVGKMDH 203
QY 86 NAKLKVAQTSVLVQ--NVSVILCGIILMMVFLHKLHLLTMVHGWLTSYVILITIANIAN 144
Db 204 FPRIPMYTALNAVQVGTQLISAATVIALRNLSHASTTAV---VLRPWFIALVAAGAIER 260
QY 145 LASTATAITTDRIWVWVAGEDRS-KLANNNATIRIDQLTNLTAPMAVQIMTFSPVI 203
Db 261 LAGLGVSVRERDWWVLLAGTNRPAQAQANAVLNELDLVCEVAGASVFLGLLSKYHPVT 320
QY 204 CGCFISGNLVSMCVBYVLLWKVYQKTPALAVRAGLKEETEELKQLNLHKTDEPKPLEGT 263
Db 321 CLXIASGLMTCSP-----PVLVM-----LGQL----- 342
QY 264 HLMGVKDSNIHELEHEQ-----EPTCASOM-----AEPRTFRDGVWVSYNQPVFLAGMG 313
Db 343 -----INRVSCHALDSRTATDESICADLLDVRRIVPNSLRATKHGWNEYKQQTVLPASAA 398
QY 314 LAFLYMTV-LGFDCTITGVAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCKGLVRT 372
Db 399 TVFLNFVVALPQALMTALLMHRGTSFSIVGAPSGLCISIMGLVATFISSLVKRVGILKA 458
QY 373 GLISGLAQSLCILCVISVFMGSPDLDSVSPEDIRSRFIQGESITPTKIPEITTEIY 432
Db 459 G-AAGLIFQASLLSIALTVVWAGS----- 481
QY 433 SNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLMSFDLTVTQLQENVIESERGII 492
Db 482 -----ISQTTPLLLIFLASIAL-----SRLGMSYDVVVGTVQIVQTVFASKANLI 525
QY 493 NGVQNSMYLLDLHFIWVILAPNEAFGLLLVLSVFMVGHIMYFRAQNTLG--NKL 550
Db 526 GGMVSVIASLAELVMLAMAILANDVSHFGFLAILSVSVAGAAWMFRCWLTNPTDQREL 595
QY 551 PACGP 555
Db 586 FMVDP 590

Search completed: August 17, 2004, 18:10:18
Job time : 52 secs
```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 17:56:35 ; Search time 43 Seconds  
(without alignments)  
4189.788 Million cell updates/sec

Title: US-09-715-927-6

Perfect score: 2929

Sequence: 1 MTFAGDHNRQCCGSLADY.....ACGPDAKEVRKENQANTSVV 571

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_protein.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriopl.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2929	100.0	571	4 Q9NP59	Q9np59 homo sapien
2	2921	99.7	571	4 Q81VB2	Q81vb2 homo sapien
3	2906	99.2	571	4 Q9NRL0	Q9nrl0 homo sapien
4	2618	89.4	570	11 Q9JHI9	Q9jhi9 mus musculus
5	2612.5	89.2	570	11 Q9JHP4	Q9jhp4 mus musculus
6	2600.5	88.8	570	11 Q923U9	Q923u9 rattus norv
7	1975.5	67.4	562	13 Q9JFW0	Q9jfw0 brachydanio
8	1871.5	67.3	562	13 Q919R3	Q919r3 brachydanio
9	1894.5	64.7	528	13 Q9AW23	Q9aw23 brachydanio
10	1513.5	51.7	436	13 Q9AW28	Q9aw28 brachydanio
11	1479.5	50.5	405	11 Q921C9	Q921c9 rattus norv
12	1360.5	46.4	305	11 Q9EMES	Q9emes mus musculus
13	1021.5	34.9	310	13 Q9ZZS1	Q9zzs1 brachydanio
14	859	29.3	167	4 Q9NUS1	Q9nus1 homo sapien
15	677	23.1	133	4 Q724F8	Q724f8 homo sapien
16	612.5	20.9	524	10 Q80905	Q80905 arabidopsis

17	564	19.3	498	10	Q9LZC8	Q9lzc8 arabidopsis
18	509.5	17.4	551	5	O44607	O44607 caenorhabdi
19	498	17.0	485	5	Q8IA95	Q8ia95 caenorhabdi
20	471.5	16.1	440	5	Q9BKT8	Q9bkt8 caenorhabdi
21	371	12.7	81	11	Q8BUM5	Q8bum5 mus musculu
22	301	10.3	593	10	Q8W4E7	Q8w4e7 arabidopsis
23	209.5	7.2	677	5	O01891	O01891 caenorhabdi
24	187.5	6.4	482	10	O04629	O04629 arabidopsis
25	164	5.6	37	11	Q9JIM9	Q9jim9 mus musculu
26	157	5.4	496	16	Q8G5T4	Q8g5t4 bifidobacte
27	155.5	5.3	408	16	Q8ID64	Q8id64 bacillus ce
28	141.5	4.8	415	16	Q8IQE6	Q8iqe6 bacillus an
29	140	4.8	434	16	Q8IPX7	Q8ipx7 bacillus an
30	138	4.7	408	16	Q8IQS7	Q8iqs7 bacillus an
31	135.5	4.6	412	16	Q8IYP3	Q8iyp3 ralatonia s
32	135	4.6	432	16	Q8IC83	Q8ic83 bacillus ce
33	132.5	4.5	414	16	Q8IRG3	Q8irg3 bacillus ce
34	131.5	4.5	420	16	Q8IDF6	Q8idf6 bacillus ce
35	128	4.4	1287	5	Q9V6Z6	Q9v6z6 drosophila
36	125.5	4.3	575	16	Q82JE2	Q82je2 streptomyce
37	123.5	4.2	409	16	Q97LU6	Q97lu6 clostridium
38	120.5	4.1	393	16	Q8G2C7	Q8g2c7 brucella su
39	120.5	4.1	763	16	Q8YFIS	Q8yfi5 brucella me
40	120	4.1	406	16	Q8IP31	Q8ip31 bacillus an
41	120	4.1	421	16	Q8G4V4	Q8g4v4 bifidobacte
42	120	4.1	481	5	Q9VNM1	Q9vnm1 drosophila
43	120	4.1	485	5	Q8S235	Q8s235 drosophila
44	119.5	4.1	420	16	Q8IF48	Q8if48 bacillus ce
45	119.5	4.1	949	16	Q8FTZ6	Q8ftz6 corynebacte

#### ALIGNMENTS

#### RESULT 1

Q9NP59	ID	Q9NP59	PRELIMINARY;	PRT;	571 AA.
AC	Q9NP59;				
DT	01-OCT-2000 (TREMBlrel. 15, Created)				
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Iron-regulated transporter IREG1 (Ferroporin) (Hypothetical protein)				
DE	(Solute carrier family 11 (Proton-coupled divalent metal ion				
DE	transporters), member 3).				
GN	IREG1 OR FPN1 OR DKFP586J0624.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
EX	MEDLINE=20337919; PubMed=10882071;				
RA	McKie A.T., Marciani P., Rolfs A., Brennan K., Wehr K., Barrow D.,				
RA	Miret S., Bomford A., Peters I.U., Farzanen F., Hediger M.A.,				
RA	Hentze M.W., Simpson R.J.;				
RT	"A novel duodenal iron-regulated transporter, IREG1, implicated in the				
RL	basolateral transfer of iron to the circulation.";				
RL	Mol. Cell 5:299-309(2000).				
[2]					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=20155474; PubMed=10693807;				
RA	Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moyrihan J.,				
RA	Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,				
RA	Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Falls J.,				
RA	Fleming M.D., Andrews N.C., Zon L.I.;				
RT	"Positional Cloning of Zebrafish Ferroporin1 Identifies a Conserved				
RL	Vertebrate Iron Exporter.";				
[3]					
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Uterus;				
RC	Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;				

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Strausberg R.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF231121; AAF44330.1; -

DR EMBL; AF226614; AAF36597.1; -

DR EMBL; AL136944; CAB66878.1; -

DR EMBL; BC037733; AAH37733.1; -

DR Genew; HGNC:10909; SLCA0A1

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch carrier.

DR PROSITE; PS00215; MITOCH\_CARRIER; 1.

KW Hypothetical protein.

SQ SEQUENCE 571 AA; 62542 MW; E4D6B5594C904959 CRC64;

Query Match 100.0%; Score 2929; DB 4; Length 571;  
Best Local Similarity 100.0%; Pred. No. 8.7e-220;  
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRAGDHNRQCGCGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

DB 1 MTRAGDHNRQCGCGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAYGLVWAGSVLVGAIIGDWVKNARLKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

DB 61 TAYGLVWAGSVLVGAIIGDWVKNARLKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

QY 121 LTMVHGWLTSYVILITITANTIANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

DB 121 LTMVHGWLTSYVILITITANTIANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

QY 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

DB 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

QY 241 EETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGV 300

DB 241 EETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGV 300

QY 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGIMTVAF 360

DB 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGIMTVAF 360

QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLSPEDIRSRFIQGESITP 420

DB 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTIYVNGSGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLTVTQLL 480

DB 421 TKIPEITTIYVNGSGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLISVSFVAMGHIMYFR 540

DB 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLISVSFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

DB 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

RESULT 2

Q8IVB2

ID Q8IVB2 PRELIMINARY; PRT; 571 AA.

AC Q8IVB2

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-OCT-2003 (TrEMBLrel. 23, Last sequence update)

DE Solute carrier family 11 (Proton-coupled divalent metal ion

transporters), member 3.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC035893; AAH35893.1; -

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch carrier.

DR PROSITE; PS00215; MITOCH\_CARRIER; 1.

SQ SEQUENCE 571 AA; 62482 MW; 45D6B5503C90495F CRC64;

Query Match 99.7%; Score 2921; DB 4; Length 571;  
Best Local Similarity 99.8%; Pred. No. 3.7e-219;  
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRAGDHNRQCGCGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

DB 1 MTRAGDHNRQCGCGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAYGLVWAGSVLVGAIIGDWVKNARLKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

DB 61 TAYGLVWAGSVLVGAIIGDWVKNARLKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

QY 121 LTMVHGWLTSYVILITITANTIANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

DB 121 LTMVHGWLTSYVILITITANTIANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

QY 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

DB 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

QY 241 EETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGV 300

DB 241 EETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGV 300

QY 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGIMTVAF 360

DB 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTTGYAYTQGLSGSILSLMGASAITGIMTVAF 360

QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLSPEDIRSRFIQGESITP 420

DB 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTIYVNGSGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLTVTQLL 480

DB 421 TKIPEITTIYVNGSGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLISVSFVAMGHIMYFR 540

DB 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLISVSFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

DB 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

RESULT 3

Q9NRL0

ID Q9NRL0 PRELIMINARY; PRT; 571 AA.

AC Q9NRL0

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SLC11A3 iron transporter.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347902; PubMed=10747949;
RA Abboud S., Haile D.J.;
RT "A Novel Mammalian Iron-regulated Protein Involved in Intracellular
RT Iron Metabolism.";
RL J. Biol. Chem. 275:19906-19912(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20291023; PubMed=10828623;
RA Haile D.J.;
RT "Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to
RT human chromosome 2q32 by in situ hybridization.";
RL EMBL: AF215636; AAF80986.1; -.
DR GO: GO:0005737; Cytoplasm; TAS.
DR GO: GO:0005887; C.integral to plasma membrane; TAS.
DR GO: GO:0005981; P.iron ion transporter activity; TAS.
DR GO: GO:0007345; P.embryogenesis and morphogenesis; TAS.
DR GO: GO:0006879; P.iron ion homeostasis; TAS.
DR GO: GO:0006826; P.iron ion transport; TAS.
DR InterPro: IPR001993; Mitoch carrier.
DR PROSITE: PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 571 AA; 62581 MW; 89707BFFC4A4B921 CRC64;
Query Match 99.2%; Score 2906; DB 4; Length 571;
Best Local Similarity 99.5%; Pred. No. 5.4e-218;
Matches 568; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTRAGDHNORCCGSLADYLSAKFLYLGHSLSTGDRMWHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNORCCGSLADYLSAKFLYLGHSLSTGDRMWHFAVSFLVELYGNLSLL 60
QY 61 TAVYGLVAGSVLVLGAIIGDWDVNNARLKVAQTSILVQNVSVILCGILMMVFLKH 120
Db 61 TAVYGLVAGSVLVLGDIIGDWDVNNARLKVAQTSILVQNVSVILCGILMMVFLKH 120
QY 121 LTMHGWLTSCVILLIITANTANLASTATITQORDWIVVAGDRSKLANMATIRI 180
Db 121 LTMHGWLTSCVILLIITANTANLASTATITQORDWIVVAGDRSKLANMATIRI 180
QY 181 DQLTNLAPVAGQVMTFSGPVIGGFTSGWNLVSMVCEYVLLKVKYQKTPALAVKAG 240
Db 181 DQLTNLAPVAGQVMTFSGPVIGGFTSGWNLVSMVCEYVLLKVKYQKTPALAVKAG 240
QY 241 EBETELKQLNLHKDTEPKPLEGTHLGVKDSNIHELEHEQEPTCASQMAEPFRD 300
Db 241 EBETELKQLNLHKDTEPKPLEGTHLGVKDSNIHELEHEQEPTCASQMAEPFRD 300
QY 301 SYNOPVFLAGVLAFLYMTVLGPDCTTGAYATQGLSGSILSLMGASAITGIMTV 360
Db 301 SYNOPVFLAGVLAFLYMTVLGPDCTTGAYATQGLSGSILSLMGASAITGIMTV 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMFGSPDLVSPPEDIRSRFIQES 420
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMFGSPDLVSPPEDIRSRFIQES 420
QY 421 TKIPEITTHIYNSGNSANIPTSPSPVPIISVSLFPAGVIAIRIGLWFDLTVTQL 480
Db 421 TKIPEITTHIYNSGNSANIPTSPSPVPIISVSLFPAGVIAIRIGLWFDLTVTQL 480
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTIMVILANPEAFGLLVLISVSFVAMGH 540
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTIMVILANPEAFGLLVLISVSFVAMGH 540
QY 541 FQNTLGNKLPACGPDPAKVRKENQANTSVV 571
Db 541 FQNTLGNKLPACGPDPAKVRKENQANTSVV 571
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RESULT 4  
Q9JHI9

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ID AC
Q9JHI9 PRELIMINARY; PRT; 570 AA.
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 25, Last annotation update)
DE SLC11A3 iron transporter (Ferroportin) (Solute carrier family 39
DE (iron-regulated transporter), member 1).
GN SLC40A1 OR FPN1 OR SLC39A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347902; PubMed=10747949;
RA Abboud S., Haile D.J.;
RT "A Novel Mammalian Iron-regulated Protein Involved in Intracellular
RT Iron Metabolism.";
RL J. Biol. Chem. 275:19906-19912(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20291023; PubMed=10828623;
RA Haile D.J.;
RT "Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to
RT human chromosome 2q32 by in situ hybridization.";
RL Cytogenet. Cell Genet. 88:328-329(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
MEDLINE=20155474; PubMed=10693807;
RA Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moynihan J.,
RA Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,
RA Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Pallas J.,
RA Fleming M.D., Andrews N.C., Zon L.I.;
RT "Positional Cloning of Zebrafish Ferroportin1 Identifies a Conserved
RT Vertebrate Iron Exporter.";
RL Nature 403:776-781(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF215637; AAF80987.1; -.
DR EMBL: AF226613; AAF36696.1; -.
DR EMBL: AK008700; BAE25840.1; -.
DR EMBL: BC003438; AAH03438.1; -.
DR MGD: MGI:1315204; SLC40a1.
DR GO: GO:0005381; P.iron ion transporter activity; IDA.
DR GO: GO:0006826; P.iron ion transport; IDA.
DR InterPro: IPR001993; Mitoch carrier.
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DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 570 AA; 62702 MW; 7125CC66171394A0A CRC64;

Query Match      89.4%; Score 2618.5; DB 11; Length 570;
Best Local Similarity 90.2%; Pred. No. 1.4e-195;
Matches 518; Conservative 18; Mismatches 31; Indels 7; Gaps 3;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
   |||
Db 1 MTKARDQTHQEGCCGSLANLYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
   |||

QY 61 TAVYGLVWAGSVLVLCALIGDWDVKNARKVQAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||
Db 61 TAVYGLVWAGSVLVLCALIGDWDVKNARKVQAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||

QY 121 LTMHGWLTSCVILIITITANTANLASTATAITIQRDWIVVAGEDRSKLANMATIRRI 180
   |||
Db 121 LTMHGWLTSCVILIITITANTANLASTATAITIQRDWIVVAGEDRSKLANMATIRRI 180
   |||

QY 181 DQLTNLAQVAVGOIMTFGSPVIGCGFISGNLVMCMVEYVLLWKVYOKTPALAVKAGLK 240
   |||
Db 181 DQLTNLAQVAVGOIMTFGSPVIGCGFISGNLVMCMVEYVLLWKVYOKTPALAVKAGLK 240
   |||

QY 241 EETELKQLNLHKDTEPKLEGLTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||
Db 241 EETELKQLNLHKDTEPKLEGLTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||

QY 301 SYNQVFLAGMGLAFVMTVIGFCITTGAYATQGLSGSILSLMGASAITGIMGTAVF 360
   |||
Db 301 SYNQVFLAGMGLAFVMTVIGFCITTGAYATQGLSGSILSLMGASAITGIMGTAVF 360
   |||

QY 361 TWLRRCGLVTRGLISGLAQLSCLILCVISVFMPSPLDLSVPPEDIRSRFIQGESITP 420
   |||
Db 361 TWLRRCGLVTRGLISGLAQLSCLILCVISVFMPSPLDLSVPPEDIRSRFVNPVSP 420
   |||

QY 421 -TKIPE--ITTELYMNGNSANIPEPSPESVPIISVLSLLFAGVIAARIGLWSPDLTVT 477
   |||
Db 421 TTKIPETVTTTMMHSMNSN---VHEMSTKPIPIVSLSLLFAGVIAARIGLWSPDLTVT 476
   |||

QY 478 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 537
   |||
Db 477 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 536
   |||

QY 538 YRFAQNTLGNKLFACGPDPAKVRKENQNTSVV 571
   |||
Db 537 YRFAQNTLGNQIFVCGPDEKEVTDENQNTSVV 570
   |||

RESULT 5
Q9JUKP4 PRELIMINARY; PRT; 570 AA.
AC Q9JUKP4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Iron-regulated transporter IREG1.
GN SLC40A1 OR SLC39A1 OR IREG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037919; PubMed=10882071;
RA McKie A.T., Marciani P., Rolfs A., Brennan K., Wehr K., Barrow D.,
RA Miret S., Bomford A., Peters T.J., Farzaneh F., Hediger M.A.,
RA Hentze M.W., Simpson R.J.;
RT "A novel duodenal iron-regulated transporter, IREG1, implicated in the
RT basolateral transfer of iron to the circulation.";
RL Mol. Cell 5:299-309(2000).
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR EMBL; AF231120; AAF44329.1; -.
DR MGD; MGI:1315204; Slc40a1.
DR GO; GO:0005381; F:iron ion transporter activity; IDA.
DR GO; GO:0005810; P:transport; IEA.

DR GO; GO:0006826; P:iron ion transport; IDA.
DR IncePro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 570 AA; 62656 MW; C648A6C61C51EDCD CRC64;

Query Match      89.2%; Score 2612.5; DB 11; Length 570;
Best Local Similarity 90.1%; Pred. No. 4.1e-195;
Matches 517; Conservative 18; Mismatches 32; Indels 7; Gaps 3;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
   |||
Db 1 MTKARDQTHQEGCCGSLANLYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
   |||

QY 61 TAVYGLVWAGSVLVLCALIGDWDVKNARKVQAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||
Db 61 TAVYGLVWAGSVLVLCALIGDWDVKNARKVQAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||

QY 121 LTMHGWLTSCVILIITITANTANLASTATAITIQRDWIVVAGEDRSKLANMATIRRI 180
   |||
Db 121 LTMHGWLTSCVILIITITANTANLASTATAITIQRDWIVVAGEDRSKLANMATIRRI 180
   |||

QY 181 DQLTNLAQVAVGOIMTFGSPVIGCGFISGNLVMCMVEYVLLWKVYOKTPALAVKAGLK 240
   |||
Db 181 DQLTNLAQVAVGOIMTFGSPVIGCGFISGNLVMCMVEYVLLWKVYOKTPALAVKAGLK 240
   |||

QY 241 EETELKQLNLHKDTEPKLEGLTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||
Db 241 EETELKQLNLHKDTEPKLEGLTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||

QY 301 SYNQVFLAGMGLAFVMTVIGFCITTGAYATQGLSGSILSLMGASAITGIMGTAVF 360
   |||
Db 301 SYNQVFLAGMGLAFVMTVIGFCITTGAYATQGLSGSILSLMGASAITGIMGTAVF 360
   |||

QY 361 TWLRRCGLVTRGLISGLAQLSCLILCVISVFMPSPLDLSVPPEDIRSRFIQGESITP 420
   |||
Db 361 TWLRRCGLVTRGLISGLAQLSCLILCVISVFMPSPLDLSVPPEDIRSRFVNPVSP 420
   |||

QY 421 -TKIPE--ITTELYMNGNSANIPEPSPESVPIISVLSLLFAGVIAARIGLWSPDLTVT 477
   |||
Db 421 TTKIPETVTTTMMHSMNSN---VHEMSTKPIPIVSLSLLFAGVIAARIGLWSPDLTVT 476
   |||

QY 478 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 537
   |||
Db 477 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 536
   |||

QY 538 YRFAQNTLGNKLFACGPDPAKVRKENQNTSVV 571
   |||
Db 537 YRFAQNTLGNQIFVCGPDEKEVTDENQNTSVV 570
   |||

RESULT 6
Q923U9 PRELIMINARY; PRT; 570 AA.
AC Q923U9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferroportin 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RA Yeh K.-Y., Yeh M., Glass J.;
RT "Iron induces ferroportin 1 (Fp1) clustering and redistribution in
RT rat intestinal epithelial cells.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394785; AAK77858.2; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
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```
DR InterPro; IPR001993; Mitochondrial carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 570 AA; 62586 MW; 766786F22F054E94 CRC64;

Query Match      88.8%; Score 2600.5; DB 11; Length 570;
Best Local Similarity 89.9%; Pred. No. 3.5e-194;
Matches 514; Conservative 19; Mismatches 36; Indels 3; Gaps 2;

QY 1 MTRAGDHNQRGCGSLADYLSAKFLLYLGHSLSTWGRMMHFAVSVFLVLYGNSLL 60
DB 1 MTKSRDTHQEGCGSLANLYLSAKFLLYLGHSLSTWGRMMHFAVSVFLVLYGNSLL 60
QY 61 TAYGLVAVAGSVLAVGALIGDWVKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLH 120
DB 61 TAYGLVAVAGSVLAVGALIGDWVKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLH 120
QY 121 LTMHGVLTSCYILITITIANIANLASTATAITIQRDWVWVAGDRSKLANNNATIRRI 180
DB 121 LNMHGVLTSCYILITITIANIANLASTATAITIQRDWVWVAGDRSKLANNNATIRRI 180
QY 181 DQNTNIALPMAVGQIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLK 240
DB 181 DQNTNIALPMAVGQIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLK 240
QY 241 EETELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGVW 300
DB 241 VESELKQNTSPADIEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGVW 300
QY 301 SYNQVQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360
DB 301 SYNQVQVFLAGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVA 360
QY 361 TWLRKCGVLRGLTSLGALQSLCLICVSVMPGSPDLSPEDIRSRPIQGESI-T 419
DB 361 TWLRKCGVLRGLTSLGALQSLCLICVSVMPGSPDLSPEDIRSRPIQGESI-T 419
QY 420 PTXKIPITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLT 479
DB 420 PTXKIPITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLT 479
QY 480 LQENVIESRGIINGVQNSMNYLLDLHFIWILAPNPAFGLLVLSVSVFAMGHIMYF 539
DB 479 LQENVIESRGIINGVQNSMNYLLDLHFIWILAPNPAFGLLVLSVSVFAMGHIMYF 539
QY 540 RPAQNTLGNKLPACGPDAKEVRKENCANTSVV 571
DB 539 RPAQNTLGNKLPACGPDAKEVRKENCANTSVV 570

RESULT 7
Q8JFWO PRELIMINARY; PRT; 562 AA.
AC Q8JFWO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SI:d22i1013.7 (Solute carrier family 39 (Iron-regulated transporter), member 1).
DE NCBI_TaxID=7955;
GN SLC39A1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Babage A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591593; CAD43474.1; -.
SQ SEQUENCE 562 AA; 61761 MW; 35CB30971553718F CRC64;

Query Match      67.4%; Score 1975.5; DB 13; Length 562;
Best Local Similarity 71.0%; Pred. No. 1.8e-145;

Matches 394; Conservative 64; Mismatches 72; Indels 25; Gaps 10;

QY 14 CGSLADYLSAKFLLYLGHSLSTWGRMMHFAVSVFLVLYGNSLLTAYVGLVAVAGSVL 73
DB 11 CERPREFFKSAFLIYVGHSLSTWGRMMHFAVSVFLVLYGNSLLTAYVGLVAVAGSVL 70
QY 74 VLGAIGDWVVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLHLLTMHGVLTSCY 133
DB 71 LGAIGDWVVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLHLLTMHGVLTSCY 130
QY 134 ILITITIANIANLASTATAITIQRDWVWVAGDRSKLANNNATIRRIIDQNTNIALPMAVG 193
DB 131 IMVITIANIANLASTATAITIQRDWVWVAGDRSKLANNNATIRRIIDQNTNIALPMAVG 190
QY 194 QIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLKE-EETELKQNLN 252
DB 191 QIMAFGSHFICGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLKE-EETELKQNLN 250
QY 253 KD---TEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGVSVYVQVFL 309
DB 251 KEIGNTE-SEVEASQLM-----TESSEPKKDTGCCYQMAEPIRTFKDGVVAYVQSIFF 303
QY 310 AGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVAFTWLRKCGL 369
DB 304 AGMGLAFYMTVLGFCITTGAYATQGLSGSILSLMGASAITGIMGTVAFTWLRKCGL 363
QY 370 VRTGLSGLAQLSCLICVSVMPGSPDLSPEDIRSRPIQGESI-TTPKIP 425
DB 364 IRTGFIAGVTQLSCLICVSVMPGSPDLSPEDIRSRPIQGESI-TTPKIP 421
QY 426 ITTEIYMSNGSANSI-VPEPSPEVPIISVSLFAGVIAARIGLWSPDLT 484
DB 422 -TTEPPI-----QANTVFEAPVESYMSVGLLPAAGVIAARIGLWSPDLT 475
QY 485 IESERGIINGVQNSMNYLLDLHFIWILAPNPAFGLLVLSVSVFAMGHIMYFPAQN 544
DB 476 IESERGIINGVQNSMNYLLDLHFIWILAPNPAFGLLVLSVSVFAMGHIMYFPAQN 535
QY 545 TLGNKFLA-CGPDAK 558
DB 536 SLGRUFLFCSPQK 550

RESULT 8
Q919R3 PRELIMINARY; PRT; 562 AA.
AC Q919R3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ferroportin.
GN SLC39A1 OR FPN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=20155474; PubMed=10693807;
RA Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moynihan J.,
RA Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,
RA Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Palis J.,
RA Fleming M.D., Andrews N.C., Zon L.I.;
RP "Positional Cloning of Zebrafish Ferroportin1 Identifies a Conserved
RT Vertebrate Iron Exporter.";
RL Nature 403:776-781(2000).
DR EMBL; AF226612; AAF36695.1; -.
SQ SEQUENCE 562 AA; 61760 MW; 38A6838E2107FBAF CRC64;

Query Match      67.3%; Score 1971.5; DB 13; Length 562;
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QY 306 PVFLAGMGLAFVLYMTVLGPDCTTGYAYTQGLSGSILSLMGASAITGIMGTVAFTWLR 365
Db 174 SIFPAGMSLAFVLYMTVLGPDCTTGYAYTQGLSGSILSLMGASAVSGICGTVAFTWIRK 233
QY 366 KQGLVRLTGLISGLAQLSCLILCVISVFMFGPGLDLSVSPFFEDIRSRFIQGES----ITPT 421
Db 234 KQGLRTGTGFIAGVTQLSCLTLCVAVFAPGSPFDLSVSPFEV-LRHLFGDSGSLRESPT 292
QY 422 KIPEITTELYMNGNSANI-VPEITSPESVPIISVLLFAGVIAARIGLWSFDLTVTQLL 480
Db 293 FIP--TTEPPI-----QANVTVEAPPVESYMSVGLLFAGVIAARVGLWSFDLTVTQLI 345
QY 481 QENVIESERGLINGVQNSMNYLLDLHLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFR 540
Db 346 QENVIESERGVINGVQNSMNYLLDLHLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFR 405
QY 541 FAQNTLGNKFLA-CGPDAK 558
Db 406 FAYKSLGRLEFLFCGPEQK 424
RESULT 11
Q921C9 PRELIMINARY; PRT; 405 AA.
AC Q921C9;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DE Cell adhesion regulator.
GN CARL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang X.Z.; (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76714; AAD00260.1; -
SQ SEQUENCE 405 AA; 45145 MW; ABDF5916C43AA4DA CRC64;
Query Match 50.5%; Score 1479.5; DB 11; Length 405;
Best Local Similarity 78.4%; Pred. No. 5.5e-107;
Matches 296; Conservative 15; Mismatches 36; Indels 31; Gaps 4;
QY 1 MTRAGDNRQRGCGGLADYLSAKFLYLGLHSLSTWGDWMHFAVSFLVELYGNLSLL 60
Db 1 MTKSRDTHQEGCGGLANVLSAKFLYLGLHSLSTWGDWMHFAVSFLVELYGNLSLL 60
QY 61 TAVYGLVWAGSVLVGLGAIIGDWVKNARKVQAQTSLVYQNSVILCGIILAMVFLKHKL 120
Db 61 TAVYGLVWAGSVLVGLGAIIGDWVKNARKVQAQTSLVYQNSVILCGIILAMVFLKHKL 120
QY 121 LTMVHGWLTSCYILITITIANIANLASTATITIQDRIWVAVGDRSKLANMNAITIRI 180
Db 121 LNMVHGWLTVCYILITITIANIANLASTATITIQDRIWVAVGDRSKLANMNAITIRI 180
QY 181 DQNTNLAPVAGQINTFGSPVIGCGFTSGWNLVSMCVYVLLMKYOKTPALAVKAGLK 240
Db 181 DQNTNLAPVAGQINTFGSPVIGCGFTSGWNLVSMCVYVLLMKYOKTPALAVKAGLK 240
QY 241 EEETELKQNLNKHDKPEKPLEGTHLMGVKDSNIHEHEQEPTCASQMAEPRTFDGWV 300
Db 241 VEESELKQNTSPKDTPEKPLEGTHLMGEKDSNIRELECEQEPTCASQMAEPRTFDGWV 300
QY 301 SYYNQPVFLAGMGLAF-----LYMTVLGDCITTTG--YAYTQGLSGSILSLMGAS 349
Db 301 SYYNQPVFLAGMGLAGPPLVDSPLGLRYRHSI---CLHSGTEFWHFQCPDGSISN----- 351
QY 350 AITGIMGTVAFTWLRKCGL 369
Db 352 -----NMNNGNCGL 360
```

## RESULT 12

```
Q8BME5 PRELIMINARY; PRT; 305 AA.
AC Q8BME5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Solute carrier family 39
GN SLC40A1 OR SLC39A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK032732; BAC28001.1; -
DR MGD; MGI:1315204; Slc40a1.
DR GO; GO:0005381; P:Iron ion transporter activity; IDA.
DR GO; GO:0006826; P:Iron ion transport; IDA.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR SEQUENCE 305 AA; 33574 MW; EC9FE6264AF4D887 CRC64;
Query Match 46.4%; Score 1360.5; DB 11; Length 305;
Best Local Similarity 88.0%; Pred. No. 7.2e-98;
Matches 272; Conservative 11; Mismatches 19; Indels 7; Gaps 3;
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QY 266 MGVDKSNHEHEQEPTCASQMAEPRTFRDGVSYNQPVFLAGMGLAFVLYMTVLGFD 325
Db 1 MGEKDSNIRELECEQEPTCASQMAEPRTFRDGVSYNQPVFLAGMGLAFVLYMTVLGFD 60
QY 326 CITTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQLSCL 385
Db 61 CITTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQLSCL 120
QY 386 LCVISVFMFGPGLDLSVSPFFEDIRSRFIQGESITP-TKIPE--ITTEIYMSGNSANIV 442
Db 121 LCVISVFMFGPGLDLSVSPFFEDIRSRFVNVEVSPPTKIPETVFTTEMENWSN---V 176
QY 443 PETSPSPVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIESERGLINGVQNSMNYL 502
Db 177 HEMSTRKPIVSVSLFAGVIAARIGLWSFDLTVTQLQENVIESERGLINGVQNSMNYL 236
QY 503 LDLLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFRAQNTLGNKLFACGPDKEVRK 562
Db 237 LDLLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFRAQNTLGNKLFACGPDKEVTD 296
QY 563 ENQNTSVV 571
Db 297 ENQNTSVV 305
```

## RESULT 13

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Q7Z251 PRELIMINARY; PRT; 310 AA.
AC Q7Z251;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE SI:d246122.1 (Solute carrier family 39 (Iron-regulated transporter), member 1) (Fragment).
GN SLC39A1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

